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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/057,275

DATE: 04/17/2002

TIME: 16:20:49

Input Set : N:\Crf3\RULE60\10057275.raw

Output Set: N:\CRF3\04172002\J057275.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Coleman, Roger
6 Bandman, Olga
7 Wilde, Craig G.
9 (ii) TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
11 (iii) NUMBER OF SEQUENCES: 11
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15 (B) STREET: 3174 Porter Drive
16 (C) CITY: Palo Alto
17 (D) STATE: CA
18 (E) COUNTRY: U.S.
19 (F) ZIP: 94304
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Diskette
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: DOS
25 (D) SOFTWARE: FastSEQ Version 1.5
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/10/057,275
C--> 29 (B) FILING DATE: 25-Jan-2002
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: US/08/390,740A
34 (B) FILING DATE: February 17, 1995
38 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: Luther, Barbara J.
40 (B) REGISTRATION NUMBER: 33,954
41 (C) REFERENCE/DOCKET NUMBER: PF-0027 US
43 (ix) TELECOMMUNICATION INFORMATION:
44 (A) TELEPHONE: 415-855-0555
45 (B) TELEFAX: 415-852-0195
48 (2) INFORMATION FOR SEQ ID NO: 1:
50 (i) SEQUENCE CHARACTERISTICS:
51 (A) LENGTH: 289 base pairs
52 (B) TYPE: nucleic acid
53 (C) STRANDEDNESS: single
54 (D) TOPOLOGY: linear
56 (ii) MOLECULE TYPE: cDNA
58 (vii) IMMEDIATE SOURCE:
59 (A) LIBRARY: Human Pancreas
60 (B) CLONE: 223187
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ENTERED

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64 ATGAAGGTCT CCGCAGCACT TCTGTGGCTG CTGCTCATAG CAGCTGCCTT CAGCCCCCAG      60
65 GGGCTCACTG GGCCAGCTTC TGTCCCAACC ACCTGCTGCT TTAACCTGGC CAATAGGAAG      120
66 ATACCCCTTC AGCGACTAGA GAGCTACAGG AGAATCACCA GTGGCAAATG TCCCCAGAAA      180
67 GCTGTGATCT TCAAGACCAA ACTGGCCAAG GATATCTGTG CCGACCCCAA GAAGAAGTGG      240
68 GTGCAGGATT CCATGAAGTA TCTGGACCAA AAATCTCCAA CTCCAAAGC      289

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71 (2) INFORMATION FOR SEQ ID NO: 2:

73 (i) SEQUENCE CHARACTERISTICS:

74 (A) LENGTH: 97 amino acids

75 (B) TYPE: amino acid

76 (C) STRANDEDNESS: single

77 (D) TOPOLOGY: linear

79 (ii) MOLECULE TYPE: peptide

81 (vii) IMMEDIATE SOURCE:

82 (A) LIBRARY: Human Pancreas

83 (B) CLONE: 223187

85 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

87 Met Lys Val Ser Ala Ala Leu Leu Trp Leu Leu Leu Ile Ala Ala Ala

88 1 5 10 15

89 Phe Ser Pro Gln Gly Leu Thr Gly Pro Ala Ser Val Pro Thr Thr Cys

90 20 25 30

91 Cys Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser

92 35 40 45

93 Tyr Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe

94 50 55 60

95 Lys Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp

96 65 70 75 80

97 Val Gln Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys

98 85 90 95

99 Pro

102 (2) INFORMATION FOR SEQ ID NO: 3:

104 (i) SEQUENCE CHARACTERISTICS:

105 (A) LENGTH: 402 base pairs

106 (B) TYPE: nucleic acid

107 (C) STRANDEDNESS: single

108 (D) TOPOLOGY: linear

110 (ii) MOLECULE TYPE: cDNA

112 (vii) IMMEDIATE SOURCE:

113 (A) LIBRARY: Human Pancreas

114 (B) CLONE: 226152

116 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

118 ATGGCTCAGT CACTGGCTCT GAGCCTCCTT ATCCTGGTTC TGGCCTTTGG CATCCCCCAGG 60

119 ACCCAAGGCA GTGATGGAGG GGCTCAGGAC TGTTCCTCA AGTACAGCCA AAGGAAGATT 120

120 CCCGCCAAGG TTGTCCGCAG CTACCGGAAG CAGGAACCAA GCTTAGGCTG CTCCATCCCA 180

121 GCTATCCTGT TCTTGCCCCG CAAGCGCTCT CAGGCAGAGC TATGTGCAGA CCCAAAGGAG 240

122 CTCTGGGTGC AGCAGCTGAT GCAGCATCTG GACAAGACAC CATCCCCACA GAAACCAGCC 300

123 CAGGGCTGCA GGAAGGACAG GGGGGCCTCC AAGACTGGCA AGAAAGGAAA GGGCTCCAAA 360

124 GGCTGCAAGA GGAAGGACAG GTCACAGACC CCTAAAGGGC CA 402

127 (2) INFORMATION FOR SEQ ID NO: 4:

129 (i) SEQUENCE CHARACTERISTICS:

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Input Set : N:\Crif3\RULE60\10057275.raw

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130      (A) LENGTH: 134 amino acids
131      (B) TYPE: amino acid
132      (C) STRANDEDNESS: single
133      (D) TOPOLOGY: linear
135      (ii) MOLECULE TYPE: peptide
137      (vii) IMMEDIATE SOURCE:
138          (A) LIBRARY: Human Pancreas
139          (B) CLONE: 226152
141      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
143 Met Ala Gln Ser Leu Ala Leu Ser Leu Ile Leu Val Leu Ala Phe
144 1      5      10      15
145 Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys
146      20      25      30
147 Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser Tyr
148      35      40      45
149 Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe
150      50      55      60
151 Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu
152      65      70      75      80
153 Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro
154      85      90      95
155 Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr
156      100     105     110
157 Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser
158      115     120     125
159 Gln Thr Pro Lys Gly Pro
160      130
162 (2) INFORMATION FOR SEQ ID NO: 5:
164      (i) SEQUENCE CHARACTERISTICS:
165          (A) LENGTH: 97 amino acids
166          (B) TYPE: amino acid
167          (C) STRANDEDNESS: single
168          (D) TOPOLOGY: linear
170      (ii) MOLECULE TYPE: peptide
172      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
174 Met Lys Val Ser Ala Ala Leu Leu Ala Leu Leu Ile Ala Ala Ala
175 1      5      10      15
176 Phe Cys Pro Gln Gly Leu Ala Gln Pro Asp Gly Val Asp Thr Pro Thr
177      20      25      30
178 Thr Cys Cys Phe Asn Tyr Ile Asn Arg Lys Ile Pro Arg Gln Arg Leu
179      35      40      45
180 Glu Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Ser Lys Pro Ala Val
181      50      55      60
182 Ile Phe Lys Thr Lys Arg Ala Lys Gln Val Cys Ala Asp Pro Lys Glu
183      65      70      75      80
184 Lys Trp Val Gln Asp Ser Met Lys His Leu Asp Lys Gln Thr Pro Lys
185      85      90      95
186 Pro
189 (2) INFORMATION FOR SEQ ID NO: 6:

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191      (i) SEQUENCE CHARACTERISTICS:
192          (A) LENGTH: 92 amino acids
193          (B) TYPE: amino acid
194          (C) STRANDEDNESS: single
195          (D) TOPOLOGY: linear
197      (ii) MOLECULE TYPE: peptide
199      (vii) IMMEDIATE SOURCE:
200          (A) LIBRARY: GenBank
201          (B) CLONE: MIP-1a
203      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
205 Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
206 1          5          10          15
207 Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
208          20          25          30
209 Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
210          35          40          45
211 Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
212          50          55          60
213 Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
214          65          70          75          80
215 Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
216          85          90
219 (2) INFORMATION FOR SEQ ID NO: 7:
221      (i) SEQUENCE CHARACTERISTICS:
222          (A) LENGTH: 92 amino acids
223          (B) TYPE: amino acid
224          (C) STRANDEDNESS: single
225          (D) TOPOLOGY: linear
227      (ii) MOLECULE TYPE: peptide
229      (vii) IMMEDIATE SOURCE:
230          (A) LIBRARY: GenBank
231          (B) CLONE: MIP-1b
233      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
235 Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
236 1          5          10          15
237 Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
238          20          25          30
239 Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val
240          35          40          45
241 Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val
242          50          55          60
243 Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser
244          65          70          75          80
245 Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn
246          85          90
249 (2) INFORMATION FOR SEQ ID NO: 8:
251      (i) SEQUENCE CHARACTERISTICS:
252          (A) LENGTH: 91 amino acids
253          (B) TYPE: amino acid

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254          (C) STRANDEDNESS: single
255          (D) TOPOLOGY: linear
257      (ii) MOLECULE TYPE: peptide
259      (vii) IMMEDIATE SOURCE:
260          (A) LIBRARY: GenBank
261          (B) CLONE: RANTES
263      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
265 Met Lys Val Ser Ala Ala Arg Leu Ala Val Ile Leu Ile Ala Thr Ala
266   1             5             10             15
267 Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro
268             20             25             30
269 Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys
270             35             40             45
271 Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe
272             50             55             60
273 Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp
274             65             70             75             80
275 Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser
276             85             90
278 (2) INFORMATION FOR SEQ ID NO: 9:
280      (i) SEQUENCE CHARACTERISTICS:
281          (A) LENGTH: 99 amino acids
282          (B) TYPE: amino acid
283          (C) STRANDEDNESS: single
284          (D) TOPOLOGY: linear
286      (ii) MOLECULE TYPE: peptide
288      (vii) IMMEDIATE SOURCE:
289          (A) LIBRARY: GenBank
290          (B) CLONE: MCP-1
292      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
294 Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr
295   1             5             10             15
296 Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val
297             20             25             30
298 Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
299             35             40             45
300 Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
301             50             55             60
302 Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
303             65             70             75             80
304 Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
305             85             90             95
306 Pro Lys Thr
309 (2) INFORMATION FOR SEQ ID NO: 10:
311      (i) SEQUENCE CHARACTERISTICS:
312          (A) LENGTH: 77 amino acids
313          (B) TYPE: amino acid
314          (C) STRANDEDNESS: single
315          (D) TOPOLOGY: linear

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/057,275

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Input Set : N:\Crf3\RULE60\10057275.raw

Output Set: N:\CRF3\04172002\J057275.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]